

## **Supplemental Material to:**

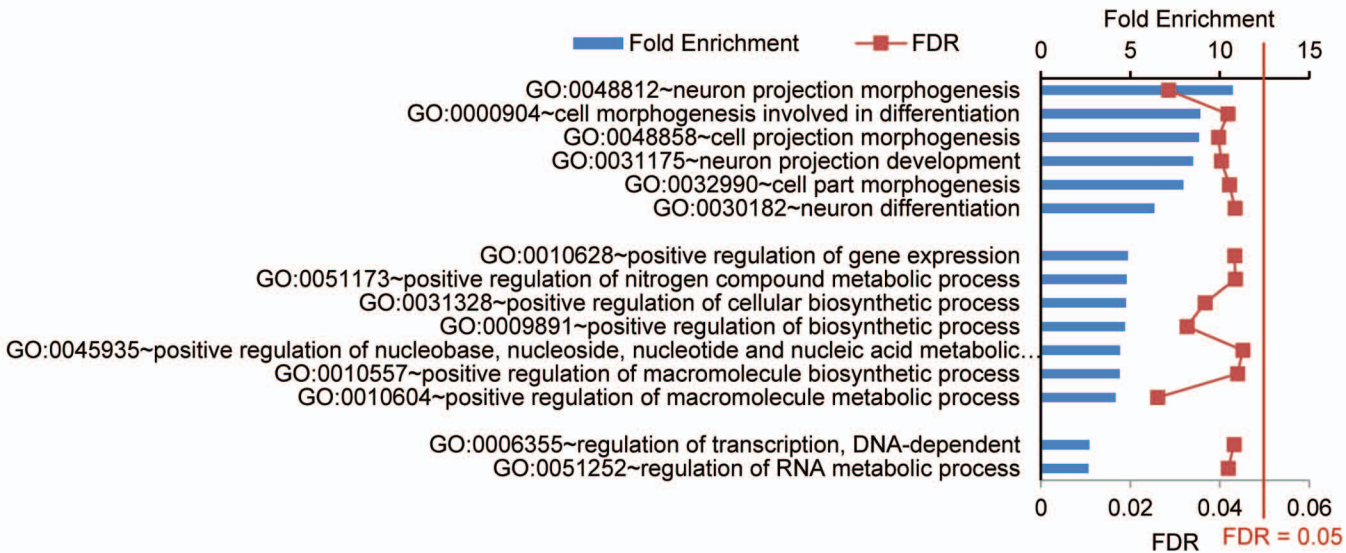
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**FUS-regulated RNA Metabolism and DNA Damage Repair:  
Implications for Amyotrophic Lateral Sclerosis and  
Frontotemporal Dementia Pathogenesis**

**2014; 2**

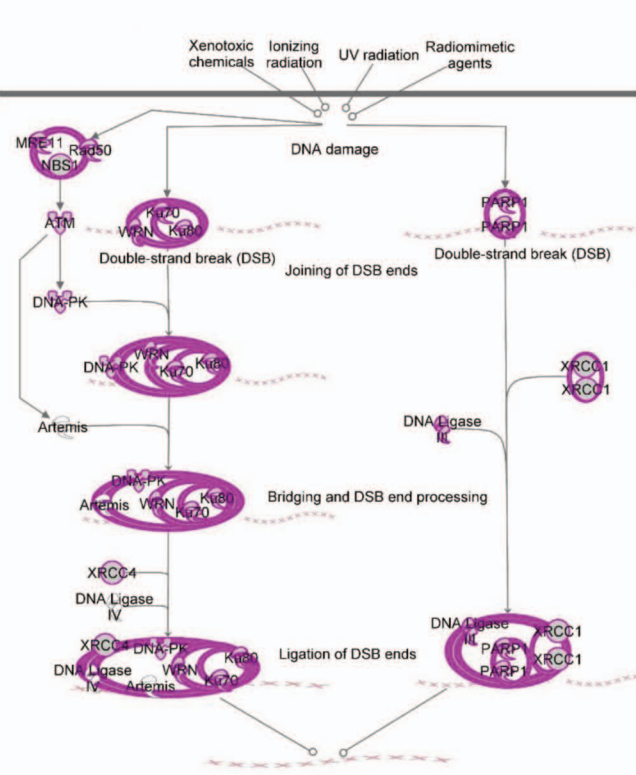
**<http://dx.doi.org/10.4161/rarediseases.29515>**

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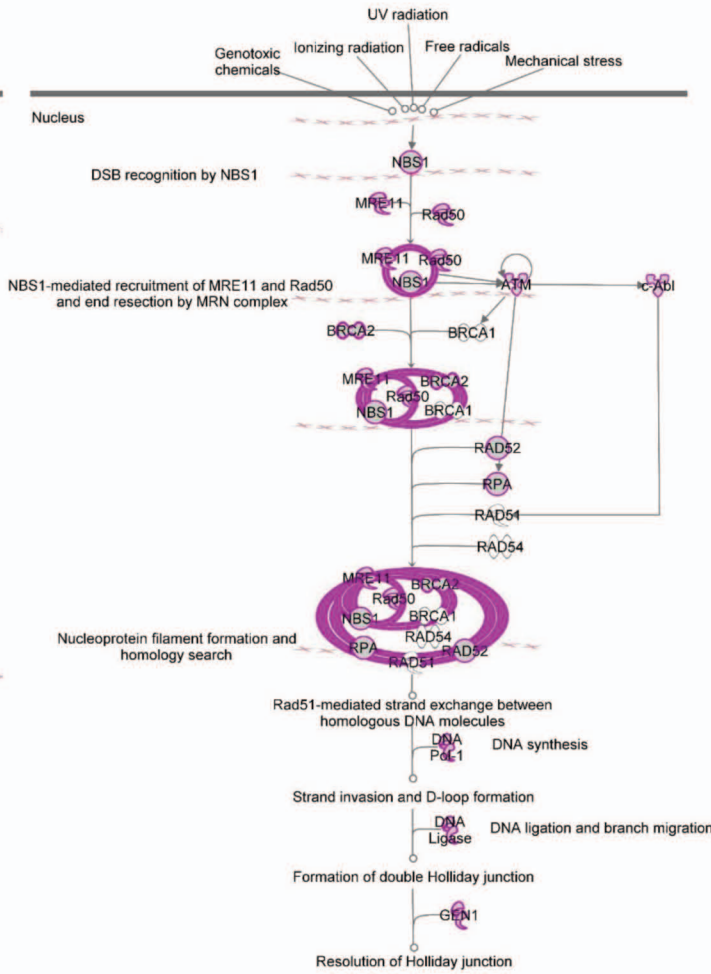
A

# NHEJ



B

# HR



**Figure S1. Clustering of Gene Ontology (GO) Biological Process terms of genes encoding FUS-associated long introns.** The analysis was performed using the DAVID Bioinformatics Resources 6.7. Analysis shows an enrichment of neurogenesis and transcription regulation. A blue bar corresponds to the number of genes that fall into a GO term. The red line represents P values.  $P \leq 0.05$  is considered strongly enriched in the annotation categories.

**Figure S2. FUS RNA targets that are mapped to DNA double-strand break repair by non-homologous end joining (NHEJ) and homologous recombination (HR) by IPA analysis.** FUS RNA targets from our<sup>12</sup> and five others' CLIP-seq assays were analyzed<sup>18-22</sup>. The RNA targets that fall into the GO: 006974 category and were also identified by at least two research groups are used for IPA. FUS RNA targets are highlighted in purple. A) NHEJ pathway. B) HR pathway.